

SEQUENCE LISTING

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<120> METHODS FOR HIGH-TEMPERATURE HYDROLYSIS OF GALACTOSE-CONTAINING
 OLIGOSACCHARIDES IN COMPLEX MIXTURES

<130> 9207.4

<150> US 60/220,211

<151> 2000-07-22

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1659

<212> DNA

<213> Thermotoga maritima

<220>

<221> CDS

<222> (1)..(1659)

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 gag aaa aac ttc aca gtt gag ttc gcg gtg gag aag ata cac ctt ggc	96
Glu Lys Asn Phe Thr Val Glu Phe Ala Val Glu Lys Ile His Leu Gly	
20 25 30	
 tgg aag atc tcc ggc agg gtg aag gga agt ccg gga agg ctt gag gtt	144
Trp Lys Ile Ser Gly Arg Val Lys Gly Ser Pro Gly Arg Leu Glu Val	
35 40 45	
 ctt cga acg aaa gca ccg gaa aag gta ctt gtg aac aac tgg cag tcc	192
Leu Arg Thr Lys Ala Pro Lys Val Leu Val Asn Asn Trp Gln Ser	
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 tgg gga ccg tgc agg gtg gtc gat gcc ttt tct ttc aaa cca cct gaa	240
Trp Gly Pro Cys Arg Val Val Asp Ala Phe Ser Phe Lys Pro Pro Glu	
65 70 75 80	
 ata gat ccg aac tgg aga tac acc gct tcg gtg gtg ccc gat gta ctt	288
Ile Asp Pro Asn Trp Arg Tyr Thr Ala Ser Val Val Pro Asp Val Leu	
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[illegible]

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340 345 350	
gag acg atc aga aaa gcg gtg gga gaa gat tct ttc atc ctc gga tgc	1104
Glu Thr Ile Arg Lys Ala Val Gly Glu Asp Ser Phe Ile Leu Gly Cys	
355 360 365	
ggc tct ccc ctt ctt ccc gca gtg gga tgc gtc gac ggg atg agg ata	1152
Gly Ser Pro Leu Leu Pro Ala Val Gly Cys Val Asp Gly Met Arg Ile	
370 375 380	
gga cct gac act gcg ccg ttc tgg gga gaa cat ata gaa gac aac gga	1200
Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly	
385 390 395 400	
gct ccc gct gca aga tgg gcg ctg aga aac gcc ata acg agg tac ttc	1248
Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe	
405 410 415	
atg cac gac agg ttc tgg ctg aac gac ccc gac tgt ctg ata ctg aga	1296
Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg	
420 425 430	
gag gag aaa acg gat ctc aca cag aag gaa aag gag ctc tac tcg tac	1344
Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr	
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acg tgt gga gtg ctc gac aac atg atc ata gaa agc gat gat ctc tcg	1392
Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser	
450 455 460	
ctc gtc aga gat cat gga aaa aag gtt ctg aaa gaa acg ctc gaa ctc	1440
Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu	
465 470 475 480	
ctc ggt gga aga cca cgg gtt caa aac atc atg tcg gag gat ctg aga	1488
Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg	
485 490 495	
tac gag atc gtc tcg tct ggc act ctc tca gga aac gtc aag atc gtg	1536
Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val	
500 505 510	
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Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser	
515 520 525	
tcc ctg aaa aaa aga gtc gtc aaa aga gaa gac gga aga aac ttc tac	1632
Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr	
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<212> PRT

<213> Thermotoga maritime

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Trp Lys Ile Ser Gly Arg Val Lys Gly Ser Pro Gly Arg Leu Glu Val
35 40 45

Leu Arg Thr Lys Ala Pro Glu Lys Val Leu Val Asn Asn Trp Gln Ser
50 55 60

Trp Gly Pro Cys Arg Val Val Asp Ala Phe Ser Phe Lys Pro Pro Glu
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Ile Asp Pro Asn Trp Arg Tyr Thr Ala Ser Val Val Pro Asp Val Leu
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Glu Arg Asn Leu Gln Ser Asp Tyr Phe Val Ala Glu Glu Gly Lys Val
100 105 110

Tyr Gly Phe Leu Ser Ser Lys Ile Ala His Pro Phe Phe Ala Val Glu
115 120 125

Asp Gly Glu Leu Val Ala Tyr Leu Glu Tyr Phe Asp Val Glu Phe Asp
130 135 140

Asp Phe Val Pro Leu Glu Pro Leu Val Val Leu Glu Asp Pro Asn Thr
145 150 155 160

Pro Leu Leu Leu Glu Lys Tyr Ala Glu Leu Val Gly Met Glu Asn Asn
165 170 175

Ala Arg Val Pro Lys His Thr Pro Thr Gly Trp Cys Ser Trp Tyr His
180 185 190

Tyr Phe Leu Asp Leu Thr Trp Glu Glu Thr Leu Lys Asn Leu Lys Leu
195 200 205

Ala Lys Asn Phe Pro Phe Glu Val Phe Gln Ile Asp Asp Ala Tyr Glu
210 215 220

Lys Asp Ile Gly Asp Trp Leu Val Thr Arg Gly Asp Phe Pro Ser Val
225 230 235 240

Glu Glu Met Ala Lys Val Ile Ala Glu Asn Gly Phe Ile Pro Gly Ile
245 250 255

Trp Thr Ala Pro Phe Ser Val Ser Glu Thr Ser Asp Val Phe Asn Glu
260 265 270

His Pro Asp Trp Val Val Lys Glu Asn Gly Glu Pro Lys Met Ala Tyr
 275 280 285
 Arg Asn Trp Asn Lys Lys Ile Tyr Ala Leu Asp Leu Ser Lys Asp Glu
 290 295 300
 Val Leu Asn Trp Leu Phe Asp Leu Phe Ser Ser Leu Arg Lys Met Gly
 305 310 315 320
 Tyr Arg Tyr Phe Lys Ile Asp Phe Leu Phe Ala Gly Ala Val Pro Gly
 325 330 335
 Glu Arg Lys Lys Asn Ile Thr Pro Ile Gln Ala Phe Arg Lys Gly Ile
 340 345 350
 Glu Thr Ile Arg Lys Ala Val Gly Glu Asp Ser Phe Ile Leu Gly Cys
 355 360 365
 Gly Ser Pro Leu Leu Pro Ala Val Gly Cys Val Asp Gly Met Arg Ile
 370 375 380
 Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly
 385 390 395 400
 Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe
 405 410 415
 Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg
 420 425 430
 Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr
 435 440 445
 Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser
 450 455 460
 Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu
 465 470 475 480
 Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg
 485 490 495
 Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val
 500 505 510
 Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser
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 Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr
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 Phe Tyr Glu Glu Gly Glu Arg Glu
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